

Appln. No. 09/736,076
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Amendments to the Claims:

This listing of the claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1 (Currently Amended). A method according in accordance with Claim 42, wherein ~~peptide comprising a peptide derivative of the HJ loop of a serine/threonine kinase, wherein:~~

~~_____ a) said peptide has between about five and about twenty amino acids or amino acid analogs; said peptide modulates activity of the serine/threonine kinase; and said peptide is cyclic.~~

~~_____ b) said peptide modulates activity of the serine/threonine kinase; and~~

~~_____ c) said peptide is cyclic.~~

2 (Currently Amended). A method in accordance with Claim 42, wherein ~~peptide comprising a peptide derivative of the HJ loop of a serine/threonine kinase, wherein:~~

~~_____ a) said peptide has between about five and about twenty amino acids or amino acid analogs;~~

~~_____ b) said peptide modulates the activity of the serine/threonine kinase; and~~

~~_____ c) said peptide has an N-terminus and a C-terminus which are unsubstituted.~~

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3 (Currently Amended). A method in accordance with Claim 42, wherein said peptide which is an amino acid sequence or a subsequence of an HJ loop of a serine/threonine kinase, with the proviso that any one amino acid in the sequence of the peptide derivative can vary, being any amino acid or analog thereof.

4 (Currently Amended). A method in accordance with Claim 42, wherein ~~peptide comprising a peptide derivative of the HJ loop of a serine/threonine kinase, wherein:~~

~~_____ a) said peptide has between about five and about twenty amino acids or amino acid analogs,~~

~~_____ b) said peptide modulates activity of the serine/threonine kinase, and~~

~~_____ e) the serine/threonine kinase is member of a serine/threonine kinase family selected from the group of families consisting of Raf, mitogen-activated protein kinases (MAP kinases), G protein-coupled receptor kinases, or the serine/threonine kinase is selected from the group consisting of protein kinase C, cyclic AMP dependent kinase, calmodulin dependent kinase, cyclic GMP dependent protein kinase, Akt/PKB and GSK3.~~

5 (Currently Amended). The method peptide of Claim 4 wherein the serine/threonine kinase is from the Raf family

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and is selected from the group consisting of Raf-1, A-Raf and B-Raf.

6 (Currently Amended). The method peptide of Claim 4 wherein the serine/threonine kinase is a G-protein dependent kinase selected from the group consisting of P2-adrenergic receptor kinases, rhodopsin kinase and GRK4-6.

7 (Currently Amended). A method in accordance with Claim 42, wherein said peptide has having the sequence of HJ-38 (SEQ ID NO.: 13), J-41 (SEQ ID NO.: 14), J-47 (SEQ ID NO.: 20), J-48 (SEQ ID NO.: 21), J-29 (SEQ ID NO.: 22), K014H010 (SEQ ID NO.: 63), K014H111 (SEQ ID NO.: 64), K048H901 (SEQ ID NO.: 66), K098H901 (SEQ ID NO.: 67), or K107H901 (SEQ ID NO.: 68).

8 (Currently Amended). A method in accordance with Claim 42, wherein said peptide has having the sequence of HJ-38 (SEQ ID NO.: 13), J-41 (SEQ ID NO.: 14), J-47 (SEQ ID NO.: 20), J-48 (SEQ ID NO.: 21), J-29 (SEQ ID NO.: 22), K014H010 (SEQ ID NO.: 63), K014H111 (SEQ ID NO.: 64), K048H901 (SEQ ID NO.: 66), K098H901 (SEQ ID NO.: 67), or K107H901 (SEQ ID NO.: 68), with the proviso that any one amino acid residue in the peptide can vary, being any naturally occurring amino acid or analog thereof.

9 (Currently Amended). A method in accordance with Claim 42, wherein said peptide comprises comprising a sequence

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of amino acids AA₁ through AA₂₀ or a subsequence thereof
comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of
tyrosine, phenylalanine and tryptophan;

AA₂ is selected from the group consisting of
glutamine, asparagine, glutamic acid, aspartic acid and an
aliphatic, substituted aliphatic, benzyl, substituted benzyl,
aromatic or substituted aromatic ester of glutamic acid or
aspartic acid;

AA₃ is selected from the group consisting of leucine,
isoleucine, methionine and valine;

AA₄ is selected from the group consisting of leucine,
isoleucine, methionine and valine;

AA₅ is selected from the group consisting of alanine,
serine and threonine;

AA₆ is glycine or alanine;

AA₇ is selected from the group consisting of glutamic
acid, aspartic acid and an aliphatic, substituted aliphatic
benzyl, substituted benzyl, aromatic or substituted aromatic
ester of glutamic acid or aspartic acid;

AA₈ is selected from the group consisting of leucine,
isoleucine, methionine and valine;

AA₉ is proline;

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AA₁₀ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₁ is selected from the group consisting of alanine, serine and threonine;

AA₁₂ is selected from the group consisting of histidine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₄ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₅ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₆ is selected from the group consisting of arginine, N-nitroarginine, β -cycloarginine, γ -

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hydroxyarginine, N-amidinocitruline and 2-amino-4-guanidinobutanoic acid;

AA₁₇ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₈ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₉ is selected from the group consisting of leucine, isoleucine, methionine and valine; and

AA₂₀ is selected from the group consisting of leucine, isoleucine, methionine and valine.

10 (Currently Amended). The method ~~peptide~~ of Claim 9 wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence of the HJ loop of Raf (SEQ ID NO.: 1) or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

11 (Currently Amended). The method ~~peptide~~ of Claim 9 wherein the sequence AA₁ through AA₂₀ or the subsequence

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thereof corresponds to the sequence or a subsequence of the HJ loop of Raf (SEQ ID NO.: 1), with the proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

12 (Currently Amended). The method ~~peptide~~ of Claim 10 or Claim 11 wherein the peptide comprises an eight amino acid subsequence of the sequence A₁ AA₁ through AA₂₀, wherein the subsequence is selected from the group consisting of AA₃ through AA₁₀, AA₇ through AA₁₄, and AA₁₁ through AA₁₈.

13 (Currently Amended). A method in accordance with Claim 42, wherein said peptide comprises ~~comprising~~ a sequence of amino acids AA₁ through AA₂₀ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₂ is selected from the group consisting of glutamine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₄ is alanine or glycine;

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AA₅ is selected from the group consisting of alanine, leucine, isoleucine, methionine and valine;

AA₆ is glycine or alanine;

AA₇ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₈ is proline;

AA₉ is proline;

AA₁₀ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₁ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₂ is glycine or alanine;

AA₁₃ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₄ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₅ is proline;

AA₁₆ is selected from the group consisting of leucine, isoleucine, methionine and valine;

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AA₁₇ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₈ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₉ is selected from the group consisting of tyrosine, phenylalanine and tryptophan; and

AA₂₀ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid.

14 (Currently Amended). The method peptide of Claim 13 wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence of the HJ loop of cyclic AMP dependent kinase (SEQ ID NO.: 2) or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

15 (Currently Amended). The method peptide of Claim 13 wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence or a subsequence of the HJ loop of cyclic AMP dependent kinase (SEQ ID NO.: 2), with the

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proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

16 (Currently Amended). The method peptide of Claim 14 or Claim 15 wherein the peptide comprises an eight amino acid subsequence of the sequence AA₁ through AA₂₀, wherein the subsequence is selected from the group consisting of AA₃ through AA₁₀, AA₇ through AA₁₄ and AA₁₁ through AA₁₈.

17. A method in accordance with Claim 42, wherein said peptide comprises ~~comprising~~ a sequence of amino acids AA₁ through AA₂₀ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₂ is selected from the group consisting of glutamine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₄ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₅ is selected from the group consisting of cysteine, alanine, leucine, isoleucine, methionine and valine;

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AA₆ is glycine or alanine;

AA₇ is selected from the group consisting of histidine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₈ is selected from the group consisting of proline, alanine and serine;

AA₉ is proline;

AA₁₀ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₁ is selected from consisting of histidine, glutamine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₂ is glycine or alanine;

AA₁₃ is selected from the group consisting of glutamine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₄ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl,

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aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₅ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₆ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₇ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₈ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₉ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₂₀ is selected from the group consisting of histidine glutamic acid, and an aliphatic, substituted

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aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid.

18 (Currently Amended). The method peptide of Claim 17 wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence of the HJ loop of protein kinase C (SEQ ID NO.: 3) or a subsequence thereof, with the proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

19 (Currently Amended). The method peptide of Claim 17 wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to a sequence or a subsequence of the HJ loop of protein kinase C (SEQ ID NO.: 3), with the proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

20 (Currently Amended). The method peptide of Claim 18 or Claim 19 wherein the peptide comprises an eight amino acid subsequence of the sequence A₁ AA₁ through AA₂₀, wherein the subsequence is selected from the group consisting of AA₃ through AA₁₀, AA₇ through AA₁₄ and AA₁₁ through AA₁₈.

21 (Currently Amended). A method in accordance with Claim 42, wherein said peptide comprises comprising a sequence of amino acids AA₁ through AA₂₀ or a subsequence thereof comprising at least five amino acids, wherein:

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AA₁ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₂ is lysine or ornithine;

AA₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₄ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₅ is selected from the group consisting of arginine, N-nitroarginine, β -cycloarginine, γ -hydroxyarginine, amidinocitruline and 2-amino-4-guanidinobutanoic acid;

AA₆ is glycine or alanine;

AA₇ is histidine;

AA₈ is serine or threonine;

AA₉ is proline;

AA₁₀ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₁ is selected from the group consisting of arginine, N-nitroarginine, β -cycloarginine, γ -hydroxyarginine, amidinocitruline and 2-amino-4-guanidinobutanoic acid;

AA₁₂ is selected from the group consisting of glutamine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl,

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aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₃ is histidine;

AA₁₄ is lysine or ornithine;

AA₁₅ is serine or threonine;

AA₁₆ is lysine or ornithine;

AA₁₇ is selected from the group consisting of glutamine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₈ is lysine or ornithine;

AA₁₉ is histidine; and

AA₂₀ is selected from the group consisting of glutamine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid.

22 (Currently Amended). The method ~~peptide~~ of Claim 21, wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence of the HJ loop of bARK1.2 (SEQ ID NO:4) or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

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23 (Currently Amended). The method peptide of Claim 21, wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence or a subsequence of the HJ loop of bARK1.2 (SEQ ID NO:4), with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

24 (Currently Amended). The method peptide of Claim 22 or Claim 23 wherein the peptide comprises an eight amino acid subsequence of the sequence A₁ AA₁ through AA₂₀, wherein subsequence is selected from the group consisting of AA₃ through AA₁₀, AA₇ through AA₁₄ and AA₁₁ through AA₁₈.

25 (Currently Amended). A method in accordance with Claim 42, wherein said peptide comprises comprising a sequence of amino acids AA₁ through AA₂₀ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₂ is selected from the group consisting of glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is selected from the group consisting of leucine isoleucine, methionine and valine;

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AA₄ is selected from the group consisting of leucine
isoleucine, methionine and valine;

AA₅ is selected from the group consisting of
cysteine, serine and threonine;

AA₆ is glycine or alanine;

AA₇ is selected from the group consisting of
arginine, N-nitroarginine, β -cycloarginine, γ -hydroxyarginine,
N-amidinocitruline, 2-amino-4-guanidinobutanoic;

AA₈ is selected from the group consisting of leucine
isoleucine, methionine and valine;

AA₉ is proline;

AA₁₀ is selected from the group consisting of
tyrosine, phenylalanine and tryptophan;

AA₁₁ is selected from the group consisting of
tyrosine, phenylalanine and tryptophan;

AA₁₂ is asparagine or glutamine;

AA₁₃ is asparagine or glutamine;

AA₁₄ is selected from the group consisting of
asparatic acid, glutamic acid and an aliphatic, substituted
aliphatic, aromatic, substituted aromatic acid, benzylic or
substituted benzylic ester of aspartic acid or glutamic acid;

AA₁₅ is selected from the group consisting of lysine,
ornithine and histidine;

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AA₁₆ is selected from the group consisting of asparatic acid, glutamic acid and an aliphatic, substituted aliphatic, aromatic, substituted aromatic acid, benzylic or substituted benzylic ester of aspartic acid or glutamic acid;

AA₁₇ is selected from the group consisting of arginine, N-nitroarginine, β - cycloarginine, γ -hydroxyarginine, N-amidinocitruline, 2-amino-4-guanidinobutanoic, lysine and ornithine;

AA₁₈ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₉ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₂₀ is selected from the group consisting of asparatic acid, glutamic acid and an aliphatic, substituted aliphatic, aromatic, substituted aromatic acid, benzylic or substituted benzylic ester of aspartic acid or glutamic acid.

26 (Currently Amended). The method ~~peptide~~ of Claim 25 wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence of the HJ loop of Akt/PKB (SEQ ID NO.: 7) or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

27 (Currently Amended). The method ~~peptide~~ of Claim 25 wherein the sequence AA₁ through AA₂₀ or the subsequence

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thereof corresponds to the sequence or a subsequence of the HJ loop of Akt/PKB (SEQ ID NO.: 7), with the proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

28 (Currently Amended). The method peptide of Claim 26 or Claim 27 wherein the peptide comprises an eight amino acid subsequence of the sequence A₁ AA₁ through AA₂₀, wherein the subsequence is selected from the group consisting of AA₃ through AA₁₀, AA₇ through AA₁₄ and AA₁₁ through AA₁₈.

29 (Currently Amended). A method in accordance with Claim 42, wherein said peptide comprises ~~comprising~~ a sequence of amino acids AA₁ through AA₂₀ or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₂ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₄ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₅ is selected from the group consisting of glutamine, leucine, isoleucine, methionine and valine;

AA₆ is glycine or alanine;

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AA₇ is selected from the group consisting of
tyrosine, phenylalanine and tryptophan;

AA₈ is proline;

AA₉ is proline;

AA₁₀ is selected from the group consisting of
tyrosine, phenylalanine and tryptophan;

AA₁₁ is selected from the group consisting of
tyrosine, phenylalanine and tryptophan;

AA₁₂ is selected from the group consisting of
asparagine, glutamine, glutamic acid, aspartic acid and an
aliphatic, substituted aliphatic, benzyl, substituted benzyl,
aromatic or substituted aromatic ester of glutamic acid or
aspartic acid;

AA₁₃ is selected from the group consisting of
asparagine, glutamine, glutamic acid, aspartic acid and an
aliphatic, substituted aliphatic, benzyl, substituted benzyl,
aromatic or substituted aromatic ester of glutamic acid or
aspartic acid;

AA₁₄ is selected from the group consisting of
asparagine, glutamine, glutamic acid, aspartic acid and an
aliphatic, substituted aliphatic, benzyl, substituted benzyl,
aromatic or substituted aromatic ester of glutamic acid or
aspartic acid;

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AA₁₅ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₆ is histidine;

AA₁₇ is selected from the group consisting of arginine, N-nitroarginine, β - cycloarginine, γ -hydroxyarginine, amidinocitruline, 2-amino-4-guanidinobutanoic acid lysine and ornithine;

AA₁₈ is selected from the group consisting of lysine, ornithine, leucine, isoleucine, methionine and valine;

AA₁₉ is selected from the group consisting of tyrosine, phenylalanine and tryptophan; and

AA₂₀ is selected from the group consisting of glutamine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid.

30 (Currently Amended). The method peptide of Claim 29 wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence of the HJ loop of calmodulin dependent kinase (SEQ ID NO.: 5) or a subsequence

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thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

31 (Currently Amended). The method peptide of Claim 29 wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence or a subsequence of the HJ loop of calmodulin dependent kinase (SEQ ID NO.: 5), with the proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

32 (Currently Amended). The method peptide of Claim 30 or Claim 31 wherein the peptide comprises an eight amino acid subsequence of the sequence A₂ AA₁ through AA₂₀, wherein the subsequence is selected from the group consisting of AA₃ through AA₁₀, AA₇ through AA₁₄ and AA₁₁ through AA₁₈.

33 (Currently Amended). A method in accordance with Claim 42, wherein said peptide comprises ~~comprising~~ a sequence of amino acids AA₁ through AA₂₀ or a subsequence thereof comprising at least five amino acids, wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence of the HJ loop of polo (SEQ ID NO.: 6) or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

34 (Currently Amended). A method in accordance with Claim 42, wherein said peptide comprises ~~comprising~~ a sequence

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of amino acids AA₁ through AA₂₀ or a subsequence thereof comprising at least five amino acids, wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence or a subsequence of the HJ loop of polo (SEQ ID NO.: 6), with the proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

35 (Currently Amended). The method peptide of Claim 33 or Claim 34, wherein the peptide comprises an eight amino acid subsequence of the sequence ~~A₁~~ AA₁ through AA₂₀, wherein the subsequence is selected from the group consisting of AA₂ through AA₁₀, AA₇ through AA₁₄ and AA₁₁ through AA₁₈.

36 (Currently Amended). A method in accordance with Claim 42, wherein said peptide comprises ~~comprising~~ a sequence of amino acid residues AA₁ through AA₂₀ or a subsequence thereof comprising at least five amino acid residues, wherein:

AA₁ is alanine or glycine;

AA₂ is glutamic acid, aspartic acid or an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₃ is leucine, isoleucine, methionine or valine;

AA₄ is leucine, isoleucine, methionine or valine;

AA₅ is leucine, isoleucine, methionine or valine;

AA₆ is glycine or alanine;

AA₇ is asparagine or glutamine;

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AA₈ is proline;

AA₉ is leucine, isoleucine, methionine or valine;

AA₁₀ is tyrosine, phenylalanine and tryptophan;

AA₁₁ is proline;

AA₁₂ is glycine or alanine;

AA₁₃ is aspartic acid, glutamic acid or an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of aspartic acid or glutamic acid;

AA₁₄ is serine or threonine;

AA₁₅ is glycine or alanine;

AA₁₆ is leucine, isoleucine, methionine or valine;

AA₁₇ is glutamic acid, aspartic acid or an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₈ is asparagine or glutamate;

AA₁₉ is leucine, isoleucine, methionine or valine;

and

AA₂₀ is leucine, isoleucine, methionine or valine.

37 (Currently Amended). The method ~~peptide~~ of Claim 36, wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence of the HJ loop of GSK3 (SEQ ID NO.: 12) or a subsequence thereof, with the proviso that any two amino acids in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

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38 (Currently Amended). The method ~~peptide~~ of Claim 36, wherein the sequence AA₁ through AA₂₀ or the subsequence thereof corresponds to the sequence or a subsequence of the HJ loop of GSK3 (SEQ ID NO.: 12), with the proviso that any one amino acid in the sequence AA₁ through AA₂₀ or the subsequence thereof can vary.

39 (Currently Amended). The method ~~peptide~~ of Claim 37 or Claim 38, wherein the peptide comprises an eight amino acid subsequence of the sequence A1 through AA₂₀, wherein the subsequence is selected from the group consisting of AA₃ through AA₁₀, AA₇ through AA₁₄ and AA₁₁ through AA₁₈.

40-41 (Canceled).

42 (Original). A method of modulating the activity of a serine/threonine kinase in a subject, comprising administering a therapeutically effective amount of a peptide comprising a peptide derivative of the HJ loop of a serine/threonine kinase, wherein:

a) said peptide has between about five and about twenty amino acids or amino acid analogs; and

b) said peptide modulates activity of the serine/threonine kinase.

43 (New). The method in accordance with claim 42, wherein the peptide is linear.

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44 (New). The method in accordance with claim 43, wherein either or both the N-terminus or the C-terminus of said peptide is substituted.

45 (New). The method in accordance with claim 44, wherein the N-terminus is amidated and the C-terminus is acylated.

46 (New). The method in accordance with claim 43, wherein the serine/threonine kinase is a member of the polo serine/threonine kinase family.

47 (New). The method in accordance with claim 46, wherein the serine/threonine kinase is a member of the polo family and is selected from the group consisting of Plk, Snk and Sak.

48 (New). The method in accordance with claim 43, wherein the peptide is represented by a sequence or a subsequence of said HJ loop, wherein the subsequence has at least about five amino acids.

49 (New). The method in accordance with claim 43, wherein the peptide has the sequence of J-42 (SEQ ID NO.: 15), J-43 (SEQ ID NO.: 16), J-43.1 (SEQ ID NO.: 17), J-45 (SEQ ID NO.: 18) or J-46 (SEQ ID NO.: 19).

50 (New). The method in accordance with claim 42, wherein said peptide consists of about twenty amino acids, AA₁

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through AA₂₀, or a subsequence thereof comprising at least five amino acids, wherein:

AA₁ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₂ is selected from the group consisting of serine and threonine;

AA₃ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₄ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₅ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₆ is glycine or alanine;

AA₇ is selected from the group consisting of arginine, N-nitroarginine, β -cycloarginine, γ -hydroxyarginine, amidinocitruline, 2-amino-4-guanidinobutanoic acid lysine and ornithine;

AA₈ is proline;

AA₉ is proline;

AA₁₀ is selected from the group consisting of tyrosine, phenylalanine and tryptophan;

AA₁₁ is selected from the group consisting of asparagine, glutamine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl,

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aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₂ is serine or threonine;

AA₁₃ is serine or threonine;

AA₁₄ is selected from the group consisting of cysteine, serine and threonine;

AA₁₅ is selected from the group consisting of leucine, isoleucine, methionine and valine;

AA₁₆ is lysine or ornithine;

AA₁₇ is selected from the group consisting of glutamine, asparagine, glutamic acid, aspartic acid and an aliphatic, substituted aliphatic, benzyl, substituted benzyl, aromatic or substituted aromatic ester of glutamic acid or aspartic acid;

AA₁₈ is serine or threonine;

AA₁₉ is selected from the group consisting of tyrosine, phenylalanine and tryptophan; and

AA₂₀ is selected from the group consisting of leucine, isoleucine, methionine and valine.